```
=> d his

        (FILE 'HOME' ENTERED AT 16:53:20 ON 22 DEC 2004)

        FILE 'MEDLINE' ENTERED AT 16:53:36 ON 22 DEC 2004
L1        100313 S SPECIFIC?(3A)ANTIBOD?
L2          1669 S HUMAN(1A)(CYTOKINE# OR (GROWTH ADJ FACTOR#) OR LYMPHOKINE#)
L3             0 S L1(3A)L2
L4             3 S L1(5A)L2


        FILE 'STNGUIDE' ENTERED AT 16:57:02 ON 22 DEC 2004

        FILE 'MEDLINE' ENTERED AT 17:18:01 ON 22 DEC 2004
L5          5952 S (CROSS-REACT? OR CROSSREACT?)(2A)ANTIBOD?
L6          1793 S L1 AND L5
L7          7377 S ANTI-HUMAN
L8            33 S L6 AND L7


        FILE 'STNGUIDE' ENTERED AT 17:20:37 ON 22 DEC 2004

        FILE 'MEDLINE' ENTERED AT 17:37:07 ON 22 DEC 2004
L9           240 S RESPONS?(1A)XENOG?
L10          455 S SPECIES-SPECIFIC(2A)ANTIBOD?
L11            1 S L9 AND L10
L12        22227 S (SCID OR NUDE)(W)(MICE OR MOUSE)
L13           29 S L9 AND L12
L14           14 S L10 AND L12


        FILE 'STNGUIDE' ENTERED AT 17:39:57 ON 22 DEC 2004

        FILE 'MEDLINE' ENTERED AT 17:46:10 ON 22 DEC 2004
L15           59 S (NONCROSS-REACT? OR NON-CROSS-REACT? OR NON-CROSSREACT?)(2A)A
L16            0 S L12 AND L15

        FILE 'STNGUIDE' ENTERED AT 17:49:20 ON 22 DEC 2004
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 20:43:02 ; Search time 98.6988 Seconds
(without alignments)
890.474 Million cell updates/sec

Title: US-10-017-910-2
Perfect score: 1299
Sequence: 1 QMDPNRISEDGTHCIYRILR.........LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
		*				
1	1299	100.0	245	2	AAY17873	Human TRA
2	1299	100.0	245	6	ABU08462	Amino aci
3	1293	99.5	249	5	ABG94282	Human RAN
4	1293	99.5	249	5	ABG80594	Human rec
5	1293	99.5	249	7	ADJ82115	Protein f
6	1293	99.5	250	6	ADA50079	Human wil
7	1293	99.5	270	4	ADJ82113	Protein f
8	1293	99.5	317	2	AAW83018	Osteoclas
9	1293	99.5	317	2	AAW83195	Human ost
10	1293	99.5	317	2	AAW69957	NF-kB rec
11	1293	99.5	317	2	AAW68293	NF-kB rec
12	1293	99.5	317	2	AAE08738	Human rec
13	1293	99.5	317	3	AAY84417	Amino aci
14	1293	99.5	317	4	AAE04426	Human rec
15	1293	99.5	317	4	AAE01993	Human ful
16	1293	99.5	317	5	ABB08134	Human RAN
17	1293	99.5	317	5	AAE26103	Human RAN
18	1293	99.5	317	5	ABG31631	Human RAN
19	1293	99.5	317	5	AAU78285	Human TRA
20	1293	99.5	317	5	AAO19096	Human rec
21	1293	99.5	317	6	ABP55108	Human ost
22	1293	99.5	317	6	AAE34364	Human rec
23	1293	99.5	317	6	ABR42314	Human RAN
24	1293	99.5	317	7	ADB16988	Human rec
25	1293	99.5	317	7	ADC35204	Human TNF
26	1293	99.5	317	7	ADC73002	Human RAN
27	1293	99.5	317	7	ADC78268	Human RAN
28	1293	99.5	317	7	ABW02277	Human RAN
29	1293	99.5	317	7	ADG46723	Human RAN
30	1293	99.5	317	8	ADJ82112	Protein f
31	1293	99.5	317	7	ADM96241	Human rec
32	1290	99.3	250	6	ADA50095	Human RAN
33	1290	99.3	250	6	ADA50094	Human RAN
34	1290	99.3	250	6	ADA50102	Human RAN
35	1290	99.3	250	6	ADA50098	Human RAN
36	1289	99.2	250	6	ADA50101	Human RAN
37	1289	99.2	250	6	ADA50089	Human RAN
38	1289	99.2	250	6	ADA50086	Human RAN
39	1289	99.2	250	6	ADA50099	Human RAN
40	1288	99.2	244	5	ABG94283	Human RAN
41	1288	99.2	244	5	AAU86148	Human PRO
42	1288	99.2	244	5	AAU78286	Human TRA
43	1288	99.2	244	5	ABG80595	Human rec
44	1288	99.2	244	7	ADC78865	Human PRO
45	1288	99.2	244	7	ADJ37323	Human tum

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 1, 2004, 20:51:51 ; Search time 24.4563 Seconds
(without alignments)
664.364 Million cell updates/sec

Title: US-10-017-910-2
Perfect score: 1299
Sequence: 1 QMDPNRISEDGTHCIYRILR.........LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM protein - protein search, using sw model

Run on: November 1, 2004, 20:54:17 ; Search time 73.8057 Seconds
(without alignments)
1076.243 Million cell updates/sec

Title: US-10-017-910-2
Perfect score: 1299
Sequence: 1 QMDPNRISEDGTHCIYR1LR.........LLDPDQDATYFGAPKVRDID 245
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 1370721 seqs, 324215800 residues
Total number of hits satisfying chosen parameters: 1370721
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB_NEW.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_NEW.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Match Length	DB	DB ID	Description
1	1299	100.0	245	10	US-09-873-829-2	Sequence 2, Appli
2	1299	100.0	245	13	US-10-017-910-2	Sequence 2, Appli
3	1293	99.5	246	14	US-10-167-182-17	Sequence 17, Appl
4	1293	99.5	246	14	US-10-460-623-17	Sequence 17, Appl
5	1293	99.5	249	14	US-10-050-902-221	Sequence 221, App
6	1293	99.5	249	14	US-10-050-898-221	Sequence 221, App
7	1293	99.5	249	15	US-10-289-456-82	Sequence 82, Appl
8	1293	99.5	250	14	US-10-338-785A-1	Sequence 1, Appli
9	1293	99.5	250	16	US-10-611-363-1	Sequence 1, Appli
10	1293	99.5	270	15	US-10-289-456-80	Sequence 80, Appl
11	1293	99.5	317	9	US-09-871-856-13	Sequence 13, Appl
12	1293	99.5	317	9	US-09-871-329-7	Sequence 7, Appli
13	1293	99.5	317	9	US-09-813-329-7	Sequence 13, Appl
14	1293	99.5	317	9	US-09-957-944-6	Sequence 6, Appli
15	1293	99.5	317	9	US-09-865-363-13	Sequence 13, Appl
16	1293	99.5	317	9	US-09-877-650-13	Sequence 13, Appl
17	1293	99.5	317	10	US-09-151-071-10	Sequence 10, Appl
18	1293	99.5	317	14	US-10-218-547-22	Sequence 22, Appl
19	1293	99.5	317	14	US-10-405-878-13	Sequence 13, Appl
20	1293	99.5	317	14	US-10-167-182-11	Sequence 11, Appl
21	1293	99.5	317	14	US-10-289-456-82	Sequence 82, Appl
22	1293	99.5	317	14	US-10-460-623-11	Sequence 11, Appl
23	1293	99.5	317	15	US-10-202-062-22	Sequence 22, Appl
24	1293	99.5	317	15	US-10-664-801-2	Sequence 2, Appli
25	1293	99.5	317	16	US-10-381-160-6	Sequence 6, Appli
26	1293	99.5	317	16	US-10-799-345-12	Sequence 12, Appl
27	1293	99.5	317	17	US-10-210-951-42	Sequence 42, Appl
28	1288	99.2	244	14	US-10-050-902-222	Sequence 222, App
29	1288	99.2	244	14	US-10-050-898-222	Sequence 222, App
30	1288	99.2	244	14	US-10-211-884-42	Sequence 42, Appl
31	1288	99.2	244	14	US-10-211-884-42	Sequence 42, Appl

Result No.	Score	Query % Match	Match Length	DB	DB ID	Description
1	1293	99.5	317	3	US-08-996-139-13	Sequence 13, Appl
2	1293	99.5	317	3	US-08-995-659-13	Sequence 13, Appl
3	1293	99.5	317	3	US-09-215-649A-13	Sequence 13, Appl
4	1293	99.5	317	3	US-09-052-521C-4	Sequence 4, Appli
5	1293	99.5	317	3	US-09-577-780-13	Sequence 13, Appl
6	1293	99.5	317	3	US-09-577-800-13	Sequence 13, Appl
7	1293	99.5	317	4	US-09-466-496-13	Sequence 13, Appl
8	1293	99.5	317	4	US-09-871-856-13	Sequence 13, Appl
9	1293	99.5	317	4	US-09-871-291-13	Sequence 13, Appl
10	1293	99.5	317	4	US-09-396-937-2	Sequence 2, Appli
11	1293	99.5	317	4	US-09-877-650-13	Sequence 13, Appl
12	1293	99.5	317	4	US-09-865-363-13	Sequence 13, Appl
13	1293	99.5	317	3	US-08-996-139-11	Sequence 11, Appl
14	1108	85.3	294	3	US-08-995-659-11	Sequence 11, Appl
15	1108	85.3	294	3	US-09-215-649A-11	Sequence 11, Appl
16	1108	85.3	294	3	US-09-577-780-11	Sequence 11, Appl
17	1108	85.3	294	4	US-09-577-800-11	Sequence 11, Appl
18	1108	85.3	294	4	US-09-466-496-11	Sequence 11, Appl
19	1108	85.3	294	4	US-09-871-856-11	Sequence 11, Appl
20	1108	85.3	294	4	US-09-871-291-11	Sequence 11, Appl
21	1108	85.3	294	4	US-09-877-650-11	Sequence 11, Appl
22	1108	85.3	294	3	US-09-865-363-11	Sequence 11, Appl
23	1101	84.8	316	3	US-08-842-842-7	Sequence 7, Appl
24	1101	84.8	316	3	US-08-989-362-2	Sequence 2, Appl
25	1101	84.8	316	3	US-09-052-521C-2	Sequence 2, Appl
26	1101	84.8	316	2	US-09-671-658A-2	Sequence 2, Appl
27	1101	84.8	316	4	US-09-396-937-6	Sequence 6, Appl
28	1101	84.8	316	4	US-09-396-937-8	Sequence 8, Appli
29	767	59.0	187	4	US-09-396-937-10	Sequence 10, Appl
30	765	58.9	173	4	US-09-396-937-12	Sequence 12, Appl
31	755	58.1	173	4	US-09-396-937-14	Sequence 14, Appl
32	717.5	55.2	188	3	US-09-396-937-16	Sequence 16, Appl
33	707.5	54.5	182	4	US-09-396-937-18	Sequence 18, Appl
34	687	52.9	173	4	US-09-396-937-20	Sequence 20, Appl
35	666	51.3	173	4	US-09-632-287A-11	Sequence 11, Appl
36	414	31.9	77	4	US-09-632-287A-10	Sequence 10, Appl
37	359	27.6	77	4	US-09-320-424-11	Sequence 11, Appl
38	235.5	18.1	253	3	US-09-825-563-11	Sequence 11, Appl
39	235.5	18.1	253	3	US-09-320-424-13	Sequence 13, Appl
40	235.5	18.1	256	3	US-09-825-563-13	Sequence 13, Appl
41	235.5	18.1	256	4	US-09-320-424-13	Sequence 13, Appl
42	234.5	18.1	279	1	US-09-072-993C-3	Sequence 3, Appli
43	234.5	18.1	281	3	US-08-670-354-2	Sequence 1, Appl
44	234.5	18.1	281	3	US-08-584-031-1	Sequence 1, Appli
45	234.5	18.1	281	3	US-08-780-496-1	Sequence 1, Appli

(continued — results 32–45)

No.	Score	%	Length	DB	ID	Description
32	1288	99.2	244	14	US-10-211-858-42	Sequence 42, Appl … lymphotoxin-beta -
33	1288	99.2	244	15	US-10-289-456-81	Sequence 81, Appl … tumor necrosis fac
34	1108	85.3	294	9	US-09-871-856-11	Sequence 11, Appl … tumor necrosis fac
35	1108	85.3	294	9	US-09-865-363-11	Sequence 11, Appl … tumor necrosis fac
36	1108	85.3	294	9	US-09-871-291-11	Sequence 11, Appl … tumor necrosis fac
37	1108	85.3	294	9	US-09-877-650-11	Sequence 11, Appl … tumor necrosis fac
38	1108	85.3	294	14	US-10-405-878-11	Sequence 11, Appl … tumor necrosis fac
39	1108	85.3	294	14	US-09-957-944-8	Sequence 8, Appl … tumor necrosis fac
40	1108	85.3	316	17	US-10-799-345-10	Sequence 10, Appl … tumor necrosis fac
41	1108	85.3	316	9	US-10-167-182-16	Sequence 16, Appl … tumor necrosis fac
42	1101	84.8	244	14	US-10-460-623-16	Sequence 16, Appl … tumor necrosis fac
43	1101	84.8	247	14	US-10-050-902-223	Sequence 223, App … lymphotoxin beta -
44	1101	84.8	247	14	US-10-050-898-223	Sequence 223, App … lymphotoxin beta -
45	1101	84.8	247	15	US-10-289-456-85	Sequence 85, Appl … 125K surface antig

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OM protein - protein search, using sw model

Run on: November 1, 2004, 20:43:45 ; Search time 111.8 Seconds
                   (without alignments)
                   1260.880 Million cell updates/sec

Title: US-10-017-910-2
Perfect score: 1299
Sequence: 1 QMDPNRISEDGTHCIYRLR.........LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_02:*
                   1: uniprot_sprot:*

OM protein - protein search, using sw model

Run on: November 1, 2004, 20:51:41 ; Search time 22.2727 Seconds
                   (without alignments)
                   1058.384 Million cell updates/sec

Title: US-10-017-910-2
Perfect score: 1299
Sequence: 1 QMDPNRISEDGTHCIYRLR.........LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR.79:*
                   1: pir1:*
                   2: pir2:*
                   3: pir3:*
                   4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	156	12.0	261	2	S53090	CD40 ligand - bovi
2	153	11.8	279	2	A53062	Fas ligand - mouse
3	149	11.5	261	2	I53476	CD40 ligand - huma
4	146.5	11.3	281	2	I38707	Fas ligand - human
5	141	10.9	234	1	JH0529	tumor necrosis fac
6	140	10.8	278	2	A49266	fas ligand - rat
7	137.5	10.6	235	1	QWMSN	tumor necrosis fac
8	132.5	10.2	235	2	I54490	tumor necrosis fac
9	130.5	10.0	234	1	A25451	tumor necrosis fac
10	129.5	10.0	306	2	I49139	lymphotoxin-beta -
11	129	9.9	233	1	QWHUN	tumor necrosis fac
12	127.5	9.8	233	1	S24642	tumor necrosis fac
13	127.5	9.8	235	2	JU0029	tumor necrosis fac
14	126.5	9.7	185	2	S52715	tumor necrosis fac
15	126	9.7	232	1	S12606	tumor necrosis fac
16	126	9.7	233	1	S22052	tumor necrosis fac
17	125	9.6	193	2	S06192	tumor necrosis fac
18	124	9.5	234	1	JQ1344	tumor necrosis fac
19	117	9.0	233	1	S11688	tumor necrosis fac
20	116	8.9	244	2	A46066	lymphotoxin beta -
21	100.5	7.7	260	2	S21738	CD40 ligand - mous
22	93	7.2	639	2	A32935	protein P1 - Entam
23	93	7.2	1114	2	JH0284	125K surface antig
24	90.5	7.0	205	1	QWHUX	lymphotoxin alpha
25	88.5	6.8	450	2	S38114	hypothetical prote
26	88	6.8	160	2	T17005	major allergen Mal
27	88	6.8	202	1	B27303	tumor necrosis fac
28	87.5	6.7	367	2	AE1180	tumor necrosis fac
29	87.5	6.7	565	2	C89893	B. subtilis YxjH a
30	87.5	6.7	578	2	S51379	hypothetical prote
31	87	6.7	794	2	S73328	probable phosphoes
32	86.5	6.7	640	2	B32935	probable lipoprote
33	86.5	6.7	1302	2	C81182	hypothetical prote
34	86.5	6.7	1829	2	S35027	iron-regulated pro
35	86.5	6.6	746	2	T06017	cytotoxin RTX homo
36	86	6.5	471	2	C64765	iron-regulated pro
37	85.5	6.5	486	2	T17006	yaiT protein precu
38	85	6.5	160	2	B81086	major allergen Mal
39	84.5	6.5	397	2	G84461	125K surface antig
40	84	6.5	397	2	S03722	hypothetical prote
41	84	6.5	1151	2	PS0154	subtilisin-like pr
42	84	6.4	197	1	JH0309	DNA-directed DNA p
43	83.5	6.4	399	2	A26916	ribonucleoside-dip
44	83.5	6.4	2325	2	T15566	hypothetical prote
45	83	6.4	202	1	JN0869	tumor necrosis fac

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1293	99.5	317	1	TN11_HUMAN	O14788 h tumor nec
2	1288	99.2	244	1	BAB79693	Bab79693 homo sapi
3	1101	84.8	316	1	TN11_MOUSE	O35235 m tumor nec
4	1092	84.1	318	1	TN11_RAT	Q9ese2 r tumor nec
5	249.5	19.2	317	2	Q72YX9	Q72yx9 brachydanio
6	241	18.6	304	2	Q7T1F2	Q7t1f2 gallus gall
7	236.5	18.2	214	2	Q9DD25	Q9dd25 brachydanio
8	234.5	18.1	281	1	TN10_HUMAN	P50591 homo sapien
9	234	18.1	281	2	CAG33176	Cag33176 homo sapi
10	234	18.0	291	1	TN10_MOUSE	P50592 mus musculu
11	233	17.9	299	2	Q6DHG9	Q6dhg9 brachydanio
12	215.5	16.6	287	2	Q90WT9	Q90wt9 gallus gall
13	206	15.9	287	2	Q8K3G0	Q8k3g0 rattus norv
14	180.5	13.9	252	2	Q8K3Y8	Q8k3y8 mus musculi
15	177	13.6	95	2	Q6UWL7	Q6uwl7 homo sapien
16	177	13.6	95	2	Q6UYL3	Q6uyl3 homo sapien
17	177	13.6	95	2	AAQ88490	Aaq88490 homo sapi
18	177	13.6	95	1	AAQ89101	Aaq89101 homo sapi
19	175.5	13.5	252	2	Q80YZ0	Q80yz0 mus musculu
20	173.5	13.4	252	2	Q8K3Y7	Q8k3y7 rattus norv
21	156	12.0	261	2	TNF5_BOVIN	P51749 bos taurus
22	156	12.0	279	2	Q7TMV9	Q7tmv9 mus musculu
23	153.5	11.8	282	1	TNF6_PIG	Q9bea8 sus scrofa
24	153	11.8	279	1	TNF6_MOUSE	P41047 mus musculi
25	153	11.8	279	2	BAC30520	Bac30520 mus muscu
26	152.5	11.8	251	2	Q8NFE9	Q8nfe9 homo sapien
27	152.5	11.7	251	2	AAH69435	Aah69435 homo sapi
28	151	11.6	280	2	Q861W5	Q861w5 felis silve
29	149	11.5	261	2	Q8BDM3	Q8bdm3 aotus trivi
30	149	11.5	261	1	TNF5_CALJA	Q9bdn3 callithrix
31	149	11.5	261	1	TNF5_HUMAN	P29965 homo sapien
32	149	11.5	261	2	AAH71754	Aah71754 homo sapi
33	148	11.4	261	1	TNF5_MACMU	Q9bdc7 macaca mula
34	146.5	11.3	280	1	TNF6_MACMU	Q9myl6 macaca mula
35	146.5	11.3	281	1	TNF6_HUMAN	P48023 homo sapien
36	146.5	11.3	281	2	Aao43991	Aao43991 homo sapi
37	144.5	11.1	280	1	TNF6_CERTO	Q9bdn1 cercocebus
38	142	10.9	234	1	TNFA_CAVPO	P51435 cavia porce
39	142	10.9	272	1	TNF5_CHICK	Q9i8d8 gallus gall
40	141.5	10.9	239	1	TN14_MOUSE	O95150 mus musculi
41	141	10.9	174	1	TN15_HUMAN	Q9qyh9 mus musculu
42	141	10.9	234	1	TNFA_SHEEP	P23383 ovis aries
43	140	10.7	278	1	TNF6_RAT	P36940 rattus norv
44	139	10.7	234	1	TNFA_CAPHI	P13296 capra hircu
45	137.5	10.6	235	1	TNFA_MOUSE	P06804 mus musculu

Title: US-10-017-910-4
Perfect score: 1675
Sequence: 1 MRRASRDYGKYLRSSEEMGS...........LLDPDQDATYPGAFKYQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1675	100.0	316	2	AAW83017	Aaw83017 Osteoclas
2	1675	100.0	316	2	AAW83194	Aaw83194 Human ost
3	1675	100.0	316	2	AAW59654	Aaw59654 Amino aci
4	1675	100.0	316	2	AAY17874	Aay17874 Murine TR
5	1675	100.0	316	2	AAY91024	Aay91024 Mouse OBM
6	1675	100.0	316	3	AAY84418	Aay84418 Amino aci
7	1675	100.0	316	3	AAY84419	Aay84419 Amino aci
8	1675	100.0	316	5	AAU78289	Aau78289 Mouse TRA
9	1675	100.0	316	6	ABR42071	Abr42071 Human RAN
10	1675	100.0	316	6	ABB99477	Abb99477 Amino aci
11	1675	100.0	316	6	ABU08463	Abu08463 Amino aci
12	1675	100.0	316	6	ABR55560	Abr55560 Amino aci
13	1597	95.3	318	4	AAB82092	Aab82092 Rat osteo
14	1554	92.8	294	2	AAW69956	Aaw69956 NF-kB rec
15	1554	92.8	294	2	AAW68292	Aaw68292 NF-kB rec
16	1554	92.8	294	2	AAE08737	Aae08737 Murine re
17	1554	92.8	294	4	AAE04425	Aae04425 Murine re
18	1554	92.8	294	4	AAE01992	Aae01992 Murine RA
19	1554	92.8	294	5	AAE26102	Aae26102 Mouse RAN
20	1554	92.8	294	7	ADB16986	Adb16986 Murine re
21	1554	92.8	294	7	ADC73000	Adc73000 Murine RA
22	1554	92.8	294	7	ADC78266	Adc78266 Murine RA
23	1554	92.8	294	7	ADG46721	Adg46721 Human RA
24	1417.5	84.6	317	2	AAW83195	Aaw83195 Human ost
25	1417.5	84.6	317	2	AAW69957	Aaw69957 Human ost
26	1417.5	84.6	317	2	AAW68293	Aaw68293 NF-kB rec
27	1417.5	84.6	317	2	AAE08738	Aae08738 Human rec
28	1417.5	84.6	317	3	AAY84417	Aay84417 Amino aci
29	1417.5	84.6	317	4	AAE04426	Aae04426 Amino rec
30	1417.5	84.6	317	4	AAE01993	Aae01993 Human ful

First search listing (rows 31–45):

No.	Score	Match	Length	DB	ID	Description
31	1417.5	84.6	317	5	Abb08134	Human RAN
32	1417.5	84.6	317	5	Aae26103	Human RAN
33	1417.5	84.6	317	5	Abg31631	Human RAN
34	1417.5	84.6	317	5	Aau78285	Human TRA
35	1417.5	84.6	317	5	Aao19096	C neoform
36	1417.5	84.6	317	6	Abp55108	Human cat
37	1417.5	84.6	317	6	Aae34364	Human rec
38	1417.5	84.6	317	6	Abr42314	Human RAN
39	1417.5	84.6	317	6	Adb16988	Human rec
40	1417.5	84.6	317	7	Adc35204	Human TNF
41	1417.5	84.6	317	7	Adc73002	Human RAN
42	1417.5	84.6	317	7	Adc78268	Human RAN
43	1417.5	84.6	317	7	Abw02277	Human RAN
44	1417.5	84.6	317	7	Adg46723	Human RAN
45	1417.5	84.6	317	7	Adj82112	Protein f

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	%Match	Query Length	DB	ID	Description
1	1675	100.0	316	2	US-08-842-842-7	Sequence 7, Appli
2	1675	100.0	316	3	US-08-989-362-2	Sequence 2, Appli
3	1675	100.0	316	3	US-09-052-521C-2	Sequence 2, Appli
4	1675	100.0	316	4	US-09-671-658A-2	Sequence 2, Appli
5	1675	100.0	316	4	US-09-396-937-4	Sequence 6, Appli
6	1675	100.0	316	4	US-09-396-937-6	Sequence 6, Appli

Second search listing (rows 7–45):

No.	Score	Match	Length	DB	ID	Description
7	1554	92.8	294	3	US-08-996-139-11	Sequence 11, Appl
8	1554	92.8	294	3	US-08-995-659-11	Sequence 11, Appl
9	1554	92.8	294	3	US-09-215-649A-11	Sequence 11, Appl
10	1554	92.8	294	4	US-09-577-780-11	Sequence 11, Appl
11	1554	92.8	294	4	US-09-577-600-11	Sequence 11, Appl
12	1554	92.8	294	4	US-09-466-496-11	Sequence 11, Appl
13	1554	92.8	294	4	US-09-871-856-11	Sequence 11, Appl
14	1554	92.8	294	4	US-09-871-291-11	Sequence 11, Appl
15	1554	92.8	294	4	US-09-877-650-11	Sequence 11, Appl
16	1554	92.8	294	3	US-09-865-363-11	Sequence 11, Appl
17	1554	92.8	294	3	US-09-396-139-13	Sequence 13, Appl
18	1417.5	84.6	317	3	US-09-215-649A-13	Sequence 13, Appl
19	1417.5	84.6	317	3	US-09-052-521C-4	Sequence 4, Appl
20	1417.5	84.6	317	3	US-08-996-139-13	Sequence 13, Appl
21	1417.5	84.6	317	4	US-09-577-800-13	Sequence 13, Appl
22	1417.5	84.6	317	4	US-09-466-496-13	Sequence 13, Appl
23	1417.5	84.6	317	4	US-09-871-856-13	Sequence 13, Appl
24	1417.5	84.6	317	4	US-09-871-291-13	Sequence 13, Appl
25	1417.5	84.6	317	4	US-09-877-650-13	Sequence 13, Appl
26	1417.5	84.6	317	4	US-09-396-937-2	Sequence 2, Appl
27	1417.5	84.6	317	4	US-09-865-363-13	Sequence 13, Appl
28	1417.5	84.6	317	4	US-09-396-937-8	Sequence 8, Appl
29	852	50.9	187	4	US-09-396-937-10	Sequence 10, Appl
30	852	50.9	173	4	US-09-396-937-12	Sequence 12, Appl
31	842	50.3	173	4	US-09-396-937-14	Sequence 14, Appl
32	804.5	48.0	188	4	US-09-396-937-16	Sequence 16, Appl
33	794.5	47.4	182	4	US-09-396-937-18	Sequence 18, Appl
34	771	46.0	173	4	US-09-396-937-20	Sequence 20, Appl
35	732	43.7	173	4	US-09-632-287A-20	Sequence 20, Appl
36	422	25.2	77	4	US-09-632-287A-10	Sequence 10, Appl
37	363	21.7	77	4	US-09-632-287A-11	Sequence 11, Appl
38	258.5	15.4	279	3	US-09-072-993C-3	Sequence 3, Appl
39	258.5	15.4	281	1	US-08-670-354-2	Sequence 2, Appl
40	258.5	15.4	281	3	US-08-584-031-1	Sequence 1, Appl
41	258.5	15.4	281	3	US-08-780-496-1	Sequence 1, Appl
42	258.5	15.4	281	3	US-08-883-086-10	Sequence 10, Appl
43	258.5	15.4	281	3	US-09-320-424-2	Sequence 2, Appl
44	258.5	15.4	281	3	US-09-333-593A-6	Sequence 6, Appl
45	258.5	15.4	281	4	US-09-157-864-11	Sequence 11, Appl

Databases :

Published_Applications_AA:*
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1: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptcdata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptcdata/2/pubpaa/US09A_PUBCOMB.pep:*
11: /cgn2_6/ptcdata/2/pubpaa/US09B_PUBCOMB.pep:*
12: /cgn2_6/ptcdata/2/pubpaa/US09C_PUBCOMB.pep:*
13: /cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*
14: /cgn2_6/ptcdata/2/pubpaa/US10A_PUBCOMB.pep:*
15: /cgn2_6/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptcdata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptcdata/2/pubpaa/US10D_PUBCOMB.pep:*
18: /cgn2_6/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptcdata/2/pubpaa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptcdata/2/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1675	100.0	316	10	US-09-079-569-7	Sequence 7, Appli
2	1675	100.0	316	10	US-09-873-829-4	Sequence 4, Appli
3	1675	100.0	316	13	US-10-017-910-4	Sequence 4, Appli
4	1675	100.0	316	14	US-10-105-057-2	Sequence 2, Appli
5	1675	100.0	316	14	US-10-272-411-19	Sequence 19, Appl
6	1675	100.0	316	14	US-10-272-328A-19	Sequence 19, Appl
7	1675	100.0	316	14	US-10-326-052-2	Sequence 2, Appli
8	1675	100.0	316	14	US-10-167-182-1	Sequence 1, Appli
9	1675	100.0	316	14	US-10-460-623-1	Sequence 1, Appli
10	1675	100.0	316	16	US-10-664-801-4	Sequence 4, Appli
11	1675	100.0	316	16	US-10-664-801-6	Sequence 6, Appli
12	1668	99.6	316	9	US-09-957-944-8	Sequence 8, Appli
13	1668	99.6	316	17	US-10-799-345-10	Sequence 10, Appl
14	1554	92.8	294	9	US-09-871-856-11	Sequence 11, Appl
15	1554	92.8	294	9	US-09-865-363-11	Sequence 11, Appl
16	1554	92.8	294	9	US-09-871-291-11	Sequence 11, Appl
17	1554	92.8	294	14	US-09-877-650-11	Sequence 11, Appl
18	1554	92.8	294	14	US-10-405-878-11	Sequence 11, Appl
19	1417.5	84.6	317	9	US-09-813-329-7	Sequence 7, Appli
20	1417.5	84.6	317	9	US-09-871-856-13	Sequence 13, Appl
21	1417.5	84.6	317	9	US-09-957-944-6	Sequence 6, Appli
22	1417.5	84.6	317	9	US-09-865-363-13	Sequence 13, Appl
23	1417.5	84.6	317	9	US-09-871-291-13	Sequence 13, Appl
24	1417.5	84.6	317	9	US-09-877-650-13	Sequence 13, Appl
25	1417.5	84.6	317	14	US-10-151-071-10	Sequence 10, Appl
26	1417.5	84.6	317	14	US-10-218-547-22	Sequence 22, Appl
27	1417.5	84.6	317	14	US-10-405-878-13	Sequence 13, Appl
28	1417.5	84.6	317	14	US-10-167-182-11	Sequence 11, Appl
29	1417.5	84.6	317	14	US-10-310-793-28	Sequence 28, Appl
30	1417.5	84.6	317	14	US-10-460-623-11	Sequence 11, Appl
31	1417.5	84.6	317	15	US-10-289-456-79	Sequence 79, Appl
32	1417.5	84.6	317	15	US-10-202-062-22	Sequence 22, Appl
33	1417.5	84.6	317	16	US-10-664-801-2	Sequence 2, Appli
34	1417.5	84.6	317	16	US-10-381-160-6	Sequence 6, Appli
35	1417.5	84.6	317	17	US-10-799-345-12	Sequence 12, Appl
36	1325	79.1	249	14	US-10-338-785A-3	Sequence 3, Appli
37	1325	79.1	249	16	US-10-611-363-3	Sequence 3, Appli
38	1315	78.5	247	14	US-10-050-902-223	Sequence 223, App
39	1315	78.5	247	14	US-10-050-898-223	Sequence 223, App
40	1315	78.5	247	15	US-10-289-456-85	Sequence 85, Appl
41	1297	77.4	244	14	US-10-167-182-16	Sequence 16, Appl
42	1297	77.4	244	14	US-10-460-623-16	Sequence 16, Appl
43	1220	72.8	270	15	US-10-289-456-80	Sequence 80, Appl
44	1127	67.3	249	14	US-10-289-456-221	Sequence 221, App
45	1127	67.3	249	14	US-10-050-902-221	Sequence 221, App

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 1, 2004, 20:51:41 ; Search time 28.7273 Seconds
                                        (without alignments)
                                        1058.384 Million cell updates/sec

Title: US-10-017-910-4
Perfect score: 1675
Sequence: 1 MRRASRDYGKYLRSSEEMGS.........LLDPDQDATYFGAFKVQDID 316

Searched: 283416 seqs, 96216763 residues

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :
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1: PIR_79:*
  1: pir1:*
  2: pir2:*
  3: pir3:*
  4: pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	185.5	11.1	261	2	S53090	CD40 ligand - bovi
2	183	10.9	278	2	A49266	fas ligand - rat
3	182	10.9	279	2	A53062	fas ligand - mouse
4	173.5	10.4	281	2	I38707	Fas ligand - human
5	171.5	10.2	261	2	I53476	CD40 ligand - huma
6	157	9.4	260	2	S21738	CD40 ligand - mous
7	149	8.9	234	1	JQ1344	tumor necrosis fac
8	146.5	8.7	235	1	QWMSN	tumor necrosis fac
9	143.5	8.6	235	1	S22052	tumor necrosis fac
10	141	8.4	234	1	JH0529	tumor necrosis fac
11	140	8.3	233	1	S11688	tumor necrosis fac
12	139.5	8.3	233	1	QWHUN	tumor necrosis fac
13	137.5	8.2	234	1	A25451	tumor necrosis fac
14	135.5	8.1	235	2	I54490	tumor necrosis fac

OM protein - protein search, using sw model

Run on: November 1, 2004, 20:43:45 ; Search time 144.2 Seconds
(without alignments)
1260.880 Million cell updates/sec

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GenCore version 5.1.6

Title: US-10-017-910-4

Sequence: 1 MRRASRDYGKYLRSSEEMGS..........LLDPDQDATYFGAPKVQDID 316

Perfect score: 1675

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Database : UniProt_02:*
  1: uniprot_sprot:*
  2: uniprot_trembl:*

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1675	100.0	316	1	TN11_MOUSE	035235 m tumor nec
2	1597	95.3	318	1	TN11_RAT	Q9ese2 r tumor nec
3	1417.5	84.6	317	1	TN11_HUMAN	O14788 h tumor nec
4	1100	65.7	244	2	BAB79693	Bab79693 homo sapi
5	283	16.9	317	2	Q7ZYX9	Q7zyx9 brachydanio
6	263.5	15.7	214	2	Q9DD25	Q9dd25 brachydanio
7	261	15.6	304	2	Q7TIF2	Q7tif2 gallus gall
8	258.5	15.4	281	1	TN10_HUMAN	P50591 homo sapien
9	258.5	15.4	281	2	CAG33176	Cag33176 homo sapi
10	250	14.9	299	2	Q6DHG9	Q6dhg9 brachydanio
11	244	14.6	291	2	TN10_MOUSE	P50592 mus musculu
12	221.5	13.2	287	2	Q8K3G0	Q8k3g0 rattus norv
13	217.5	13.0	287	2	Q90WT9	Q90wt9 gallus gall
14	188.5	11.3	261	2	TNF5_CALJA	Q9bdn3 callithrix
15	185.5	11.1	252	2	Q8K3Y8	Q8k3y8 mus musculu
16	185.5	11.1	261	2	TNF5_BOVIN	P51749 bos taurus
17	185	11.0	279	2	Q7TMV9	Q7tmv9 mus musculu
18	183	10.9	278	2	TNF6_RAT	P36940 rattus norv
19	182.5	10.9	261	1	TNF5_AOTTR	Q9bdm3 aotus trivi
20	182	10.9	279	2	TNF6_MOUSE	P41047 mus musculu
21	182	10.9	279	2	BAC30520	Bac30520 mus muscu
22	180.5	10.8	252	2	Q80YZ0	Q80yz0 mus musculu
23	179.5	10.7	282	2	TNF6_PIG	Q9bea8 sus scrofa
24	178.5	10.7	280	2	Q861W5	Q861w5 felis silve
25	178	10.6	280	1	TNF6_MACMU	Q9my1.6 macaca mula
26	177	10.6	280	1	TNF6_CERTO	Q9bdn1 cercocebus
27	176.5	10.5	261	1	TNF6_MACMU	Q9bdc7 macaca mula
28	176	10.5	95	2	Q6UWL7	Q6uwl7 homo sapien
29	176	10.5	95	1	Q6UY13	Q6uy13 homo sapien
30	176	10.5	95	2	AAQ88490	Aaq88490 homo sapi
31	176	10.5	95	2	AAQ99101	Aaq99101 homo sapi
32	175.5	10.5	252	2	Q8K3Y7	Q8k3y7 rattus norv
33	173.5	10.4	281	2	TNF6_HUMAN	P48023 homo sapien
34	173.5	10.4	281	2	AAO43991	Aao43991 homo sapi
35	171.5	10.2	261	2	TNF5_HUMAN	P29965 homo sapien
36	171.5	10.2	261	2	AAH71754	Aah71754 homo sapi
37	167.5	10.0	272	2	TNF5_CHICK	Q9i8d8 gallus gall
38	164	9.8	260	1	TNF5_FELCA	Q97605 felis silve
39	159.5	9.5	261	1	TNF5_PIG	Q95mg5 sus scrofa
40	158.5	9.5	251	2	Q8NFE9	Q8nfe9 homo sapien
41	158.5	9.5	251	2	AAH69435	Aah69435 homo sapi
42	157	9.4	234	1	TNFA_CAVPO	P51435 cavia porce
43	157	9.4	260	1	TNF5_MOUSE	P27548 mus musculu
44	154	9.2	260	2	TNF5_CANFA	O97626 canis famil
45	154	9.2	260	2	AAP86654	Aap86654 canis fam

Result No.	Score	% Query Match	Length	DB	ID	Description
15	133.5	8.0	233	1	S24642	tumor necrosis fac
16	133	7.9	185	2	S52715	tumor necrosis fac
17	133	7.9	232	1	S12606	tumor necrosis fac
18	129.5	7.7	235	2	JU0029	tumor necrosis fac
19	129.5	7.7	306	2	I49139	lymphotoxin-beta -
20	117	7.0	244	2	A46066	lymphotoxin beta -
21	115.5	6.9	193	2	S06192	tumor necrosis fac
22	103.5	6.2	340	2	S49742	tumor necrosis fac
23	103	6.1	3848	2	T17414	Tipc protein - ali
24	99.5	5.9	558	2	T23649	hypothetical prote
25	99	5.9	440	2	I49681	glyceraldehyde-3-p
26	97	5.8	450	2	S38114	hypothetical prote
27	95.5	5.7	553	2	B5514	dihydrolipoamide S
28	94	5.6	1486	1	B40333	collagen alpha 1(I
29	93.5	5.6	205	1	QWMUX	lymphotoxin alpha
30	92.5	5.5	197	2	JH0309	lymphotoxin alpha
31	92	5.5	549	2	JC5926	secreted klotho pr
32	92	5.5	785	2	T23456	hypothetical prote
33	92	5.5	1012	2	JC5925	membrane klotho pr
34	90.5	5.4	658	2	T39500	serine/threonine-s
35	90.5	5.4	750	2	E84475	probable Athila re
36	90.5	5.4	952	2	AC0447	probable insectici
37	90	5.4	3011	1	S40770	genome polyprotein
38	89	5.3	1694	2	S50065	sialoadhesin - mou
39	89	5.3	202	1	B27303	tumor necrosis fac
40	88.5	5.3	477	2	I38409	adenylyl cyclase-a
41	88.5	5.3	1547	2	JQ0096	hypothetical 176K
42	88	5.3	347	2	H75253	hypothetical prote
43	88	5.3	560	1	JQ1221	probable 60K inner
44	88	5.3	1420	2	T37781	probable cytoskele
45	88	5.3	2774	2	A43359	microtubule-associ